

Figure 1A

1 CACCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGC_{cc} AAAGCTCCTC 60
 61 TGCCCACCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC T_cTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTC_t TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAG_{AA} 180
 181 AGGCCTGAAG GAACAGGCCG GGGAGGAGC CCTCCCTCTC TCCCTTGTC_c CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGCAA TACCAAAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAAC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAACATG ACGAGAGGG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 1B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCATAAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAAATC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTTG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTGCAATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCTG 2520

2521 GGCCCCTAAT CCCAGGCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGTTGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCATA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

D0053 NP

Figure 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 2A

1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCCTC 60
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGGAGGAGC CCTCCCTCTC TCCCTGTCC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTGAUTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 2B

961 GTCCCGACTG CCGTCCTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTCTTC TATTCCTACA CGCTGCTCAC AGACTCTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGTA CTGGTCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTT 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V *

2341 GCTCCCCTCA CCCTGCCTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTGCTATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCTG 2520

2521 GGCCCCTAAT CCCAGGCCCT GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGTTGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCATA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

Figure 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 3A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 3B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 4A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCCA TGAGGCCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 4B

901 TTCTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGT GGGCCAGCTC 960
299 F F A F T N S S L N P V I Y V F V G Q L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 5A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCAA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 ACCAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGGGAA GGCAGGCCCG GGTACACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACCC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCCTGGTCT GCTGGCCCC TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 5B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCCTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 6A

1 ATGTTCTCTC CCTGGAAAGAT ATCAATGTTT CTGTCCTGTC GTGAGGACTC CGTGCCCACC 60
 1 M F S P W K I S M F L S V R E D S V P T 20

 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

 121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

 181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

 241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

 301 GCAGCAGACC TGATCCTGGC CTGGGGCTG CCCCCTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

 361 TTGCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

 421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

 481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

 541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

 601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

 661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACT 720
 221 E V F T N M L L N V V G F L L P L S V I 240

 721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

 781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

 841 ATCTGCTGGC TGCCCTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 6B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCTGG GTTTCTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATT ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCAGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTG ACATGGCAAA 3180
3181 GAGCCATAA ATCCTGACCA ATCCAACTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

Figure 6D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGGGCCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAA AAA 3733

Figure 7A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 7B

961 ATTGTCTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTTC AGGATG 1766

Figure 8A

1 AATTCAGAGC CACCGCGGGC AGGCAGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTCCTCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 8B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCTTTGG CAGGTGCAGC CCCCACGTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTGGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

Figure 9A

1 AATTCAGAGC CACCGCGGGC AGGCAGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GGCAGGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
1 M D N V L P V D S D 10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300
11 L S P N I S T N T S E P N Q F V Q P A W 30

301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
31 Q I V L W A A A Y T V I V V T S V V G N 50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATT 420
51 V V V M W I I L A H K R M R T V T N Y F 70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
71 L V N L A F A E A S M A A F N T V V N F 90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCCTGTTCT ACTGCAAGTT CCACAACTTC 540
91 T Y A V H N E W Y Y G L F Y C K F H N F 110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F P I A A V F A S I Y S M T A V A F D R 130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCA CCACAGCCAC CAAAGTGGTC 660
131 Y M A I I H P L Q P R L S A T A T K V V 150

661 ATCTGTGTCA TATGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I C V I W V L A L L L A F P Q G Y Y S T 170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T E T M P S R V V C M I E W P E H P N K 190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840
191 I Y E K V Y H I C V T V L I Y F L P L L 210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V I G Y A Y T V V G I T L W A S E I P G 230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 9B

961 ATTGTGCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCTTTGG CAGGTGCAGC CCCCACGTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

Figure 10A

1 AATTCAGAGC CACCGCGGGC AGGCAGGCAG TGCATCCAGA AGCGTTATA TTCTGAGCGC 60

61 CAGTCAGCT TTCAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90

481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150

661 ATCTGTGTCA TCTGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 10B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCA C ATCTCCACA GTGGTGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCTTTGG CAGGTGCAGC CCCCACGTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

Figure 11A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GCGAAGGGAGGTCGAAAC AACAGTTATC TCCAAGATGC TATTGTTGA ACCCATCCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGGCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCAC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAAACCTGG AGAGCCTCCT CTCTTACCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 11B

961 ACAACATTTG ATCCCAGAAGAA AACCCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTGTTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGC GGAAACTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 12A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GGCGAAGGGA AGGTGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGGCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCCACCAA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTG AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 12B

961 ACAACATTTG ATCCCAAGAA AACCGAGATG GAACCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCC CTTTCATTGA CCAAACATTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACCC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 13A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCT GCTGACCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCTG 240
41 G E G K V A T T V I S K M L F A E P I L 60

241 GAGGTTTCCA GCTTGGCAG AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCC ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACAA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 13B

961 ACAACATTG ATCCCAGAA ACCAGAATG GAACCCTTC ACTTCAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTCT CTAGTTCAAG TTCACCCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 14A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCCTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGGAATG 540
 141 V L G D A L V D F S L K L Y H A F S G M 160
 541 AAGAAGGTGG AGACCAACAT GGCTTTTCC CCATTCAAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCCTGT ACAGCAGCAG CCCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 14B

961 ACAACATTTG ATCCCAAGAA AACCGAGATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCA TGATGAATAG CAAGAAAGTAC CCTGTGGCCC ATTCATTGA CCAAACTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGTAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCAGGTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACGTGACA GAGACTGGGG TGGAGGCGGC TGCAAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 15A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGGCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCCACCAA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCCCTCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 15B

961 ACAACATTTG ATCCCAAGAA AACAGAATG GAACCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAAGTCCCCA TGATGAATAG CAAGAAAGTAC CCTGTGGCCC ATTCATTGA CCAAACATTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGTAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGGCTC TCAGCCCTTC TGTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
 461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACCC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 16

1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCATGT GGTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGGT ACGACGAAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCCACCGA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACCAAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCCTA ATGATGAGTG CAAAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 17

1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCAGT GGTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATT CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGGT ACGACGAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCGA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACCAAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCCTA ATGATGAGTG CGAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C E K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 18

1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCAGTG GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCAGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACCACGAAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGAACACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCCACCA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T Q E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACCAAGAGAA TTTCTCATT 540
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCCTA ATGATGAGTG CAAAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 19

BRB1_MOUSE MASQ. **A**SLKLQPSNOSQQAPPNITSCEGAPEAWDLLCRVLPGFVIT**V**CF^{*}FG^{*}LLGNLLVLS
 BRB1_RAT MASE. V^{*}LELQPSNRS^{*}QAPPNITSCESALEDW^{*}LLYRVLPGFVITICFFG^{*}LLGNLLVLS
 BRB1_HUMAN MASSW^{*}PLELQ^{*}SNQSQLFPQNATACDNAPEAWDLLHRVLPTF^{*}I**S**ICFFG^{*}LLGNLFVLL
 BRB1_RABIT MASQ. **C**PLELQPSNQSQLAPPNATSCSGAP**A**WD^{*}LLHR**L**PTF^{*}I**A**IFT**L**GLLGNSFVLS

BRB1_MOUSE FFLLPWR^{*}WW...QQRQR^{*}LT**T**AEIYLANLAASDLVFLVGLPFWAEN**V**GNRFNWPFGSDL
 BRB1_RAT FFLLPWR^{*}WWQQRQR^{*}QQLT**T**AEIYLANLAASDLVFLVGLPFWAEN**V**GNRFNWPFGTDL
 BRB1_HUMAN VFLLP...**T**RRQLNVAE^{*}IYLANLAASDLVFLVGLPFWAEN**V**WNOFNWPFGALL
 BRB1_RABIT VFLLA...**T**RRRLSVAE^{*}IYLANLAASDLVFLVGLPFWAEN**V**RNOFDWPFGAAL

BRB1_MOUSE CRVVSGVIKANLFISIFLVVAISQDRYR**L**VYPMTSWG**N**R^{*}RRRQAQ**V**TCLLIWVAGGLS
 BRB1_RAT CRVVSGVIKANLF**S**IFLVVAISQDRYR**L**VYPMTSWG**Y**R^{*}RRRQAQ**A**TCLLIWVAGGLS
 BRB1_HUMAN CRV**T**NGVIKANLFISIFLVVAISQDRYR**V**LVHPMASGR**Q**RRRQAQ**R**VTC**M**LIWV**V**GGLLS
 BRB1_RABIT CR**V**NGVIKANLFISIFLVVAISQDRY**S**VLVHPMASRRGRRRQAQ**A**TCLLIW**V**AGGLS

BRB1_MOUSE TPTFLLRSVKVVPDLN**S**ACILLF**P**HEAWHF**V**RMVELNVLGFLPLAAIL**M**FN**E**HILASL
 BRB1_RAT IPTFLLRSVKVVPDLN**S**ACILLF**P**HEAWHFARMVELNVLGFLPL**V**TAI**F**FNYHILASL
 BRB1_HUMAN IPTFLLRS**T**QAVPDLN**T**ACILLPHEAWHFAR**E**VELN**L**GF^{*}LLPLAAI**V**FFNYHILASL
 BRB1_RABIT TPTF**M**LR^{*}SVRAV**P**ELN**S**ACILLPHEAWHF**W**LRMVELN**L**GF^{*}LLPLAAI**L**FFNC^{*}HILASL

BRB1_MOUSE RGQKEASRTRCGGP^{*}KDSKT**M****C**LILTLV^{*}ASFLV^{*}CWAPYHFFAFL**D**FLVQVRVI**Q**DCFWKBL
 BRB1_RAT RGQKEASRTRCGGP^{*}KGSKT**T****C**LILTLV^{*}ASFLV^{*}C^{*}PYHFFAFL**D**FLVQVRVI**Q**DCSWKEI
 BRB1_HUMAN RTREEVS^{*}TRVRGPKDSKT**T****A**LILTLV^{*}VAFLV^{*}CWAPYHFFAFL**E**FLFQVQAVRGCFWE**D**
 BRB1_RABIT RRRGERVP^{*}RCGGPRDSK**S****T****A**LILTLV^{*}ASFLV^{*}CWAPYHFFAFL**E**CLWQVHAIGGC^{*}WEEF

BRB1_MOUSE TDLGLQLANFFAFVNSCLNPL**I**YVFAG**L**FKTRVLGTL^{*}
 BRB1_RAT TDLGLQLANFFAFVNSCLNPL**I**YVFAG**L**LKTRVLGTL^{*}
 BRB1_HUMAN IDLGLQLANFFAFTNS^{*}SLNP**I**YVFVG**L**FRTKVWE^{*}LYKQ**C**TPKSLAF^{*}SSSHRKE**F**QL
 BRB1_RABIT TDLGLQLSNFSAFVNSCLNP**I**YVFVG**L**FRTKVWE**C**Q**S**PRSLAPV^{*}SSSRKEMLWG

BRB1_MOUSE ~~~~
 BRB1_RAT ~~~~
 BRB1_HUMAN FWRN
 BRB1_RABIT FWRN

Figure 20

BRB2_MOUSE ~~~~~MPCSWKLLGFISVHE. PMPTAAASFGIFEMFNVTTQVLGSALNGTISKDN. CPDTEW
 BRB2_RAT MDTRSSLCP. KTQAVVAVFW. GPGCHLSTCIEMFNITTQALGSAHNGTFSEVN. CPDTEW
 BRB2_RABIT ~~~~~MLNITSQVLAPALNGSVSQSSGCPNTEW
 BRB2_CAVPO ~~~~~MFNITSQV. SALNATTAQGNSCLDAEW
 BRB2_HUMAN ~~~~~MFSPWKISMFLSVREDSVPTTASFSADMLNVTLQ. GPTLNGTFAQ. SKCPQVEW

BRB2_MOUSE WSWLNAIQAPFLWVLFILAALENIFVLSVFFLHKNSCTVAEIYLGNLAADLILACGLPF
 BRB2_RAT WSWLNAIQAPFLWVLFILAALENIFVLSVFCLHKNSCTVAEIYLGNLAADLILACGLPF
 BRB2_RABIT SGWLNVIQAPFLWVLFVLATLENIFVLSVFCLHKSSCTVAEIYLGNLAADLILACGLPF
 BRB2_CAVPO WSWLNTIQAPFLWVLFVLATLENIFVLSVFFLHKSSCTVAEIYLGNLAADLILACGLPF
 BRB2_HUMAN LGWLNTIQPPFLWVLFVLATLENIFVLSVFCLHKSSCTVAEIYLGNLAADLILACGLPF

BRB2_MOUSE WAITIANNFDWVGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSGMRGVR
 BRB2_RAT WAITIANNFDWLFGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSGMRGVR
 BRB2_RABIT WATTIANNFDWLFGEALCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSGMRGVR
 BRB2_CAVPO WAITIANNFDWLFGEVLCRVNTMIQMNLYSSICFLMLVSIDRYLALVKTMSGMRGVR
 BRB2_HUMAN WAITISNNFDWLFGETLCRVVNATISMNLYSSICFLMLVSIDRYLALVKTMSGMRGVR

BRB2_MOUSE WAKLYSLVIWGCTLLSSPMLVFRTMFYSEDEGHNVTACVIYPSRSWEVFTNVLLNLVG
 BRB2_RAT WAKLYSLVIWSCTLLSSPMLVFRTMKDRDEGHNVTACVIYPSRSWEVFTNVLLNLVG
 BRB2_RABIT WAKLYSLVIWGCTLLSSPMLVFRTMKDRDEGHNVTACVIYPSRSWEVFTNVLLNLVG
 BRB2_CAVPO WAKLYSLVIWGCALLLSSPMLVFRTMKDRDEGHNVTACVIYPSLWQVFTNVLLNLVG
 BRB2_HUMAN WAKLYSLVIWGCTLLSSPMLVFRTMKDRDEGHNVTACVIYPSLWQVFTNVLLNLVG

BRB2_MOUSE FLLPLSVITFCTVRITQVLRNNEMKKFKEQTERATVVLVLAVLGLFVCWMPFQISTFL
 BRB2_RAT FLLPLSTITFCTVRIQVLRNNEMKKFKEQTERATVVLVLAVLGLFVCWPFQISTFL
 BRB2_RABIT FLLPLSVITFCTVQITQVLRNNEMQKFKEIQTERRATVVLVLAVLLLFVCWLPFQISTFL
 BRB2_CAVPO FLLPLSTITFCTVQIMQVLRNNEMQKFKEIQTERRATVVLVLAVLLLFVCWLPFQIGTFL
 BRB2_HUMAN FLLPLSVITFCTMQIMQVLRNNEMQKFKEIQTERRATVVLVLAVLLLFVCWLPFQISTFL

BRB2_MOUSE DTLLRLGVLSGCWDEHAIDVITQISSYAYNSNSCLNPLVYVIVGKFRKKSREVYRVQVCR
 BRB2_RAT DTLLRLGVLSGCWNERAVDITVITQISSYAYNSNSCLNPLVYVIVGKFRKKSREVYQAIACR
 BRB2_RABIT DTLLRLGVLSGCWDEHMIDVITQIGSEMCYAYNSNSCLNPLVYVIVGKFRKKSREVYRAACP
 BRB2_CAVPO DTLRILGFLPGCW. EHMIDITQISSYAYNSNSCLNPLVYVIVGKFRKKSREVYHGTCR
 BRB2_HUMAN DTLHRLGILSSCQDERIDVITQIASMAYNSNSCLNPLVYVIVGKFRKKSWEVYQGVQ

*

BRB2_MOUSE K GCMGEPVQMNEMSGTLLRTSISVERQIHKLQDWAGKQ~~~~~
 BRB2_RAT K GCMGESVQMNEMSGTLLRTSISVDRQIHKLQDWAGNQ~~~~~
 BRB2_RABIT KAGCVLEPVQAESSMGTLLRTSISVERQIHKLPEWTRSSQ~~~~~
 BRB2_CAVPO S GCVSEPAQSENSMGTLLRTSISVDRQIHKLQDWARSSEGTPPGLL
 BRB2_HUMAN K GCRSEPIQMENSMGTLRTSISVERQIHKLQDWAGSRO~~~~~

Figure 21A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGCCGA GNCAAGCCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATC^NTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I X L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGC^NGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V X G P K D S K T T A L I L T L V V A 258

781 TTCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 21B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGTT GGGCC**NGCTC** 960
299 F F A F T N S S L N P V I Y V F V G **X** L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 22A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

61 CAGTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTACGCC TAGCTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
1 M D N V L P V D S D 10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300
11 L S P N I S T N T S E P N Q F V Q P A W 30

301 CAAATTGTCC TTTGGGCAGC TGCCCTACAGC GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
31 Q I V L W A A A Y T V I V V T S V V G N 50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTT 420
51 V V V M W I I L A H K R M R T V T N Y F 70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480
71 L V N L A F A E A S M A A F N T V V N F 90

481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTTC 540
91 T Y A V H N E W Y Y G L F Y C K F H N F 110

541 TT~~N~~CCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F P I A A V F A S I Y S M T A V A F D R 130

601 TACATGGCCA TCATACATCC CCTCCAGGCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y M A I I H P L Q P R L S A T A T K V V 150

661 ATCTGTGTCA TNTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I C V I W V L A L L L A F P Q G Y Y S T 170

721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T E T M P S R V V C M I E W P E H P N K 190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840
191 I Y E K V Y H I C V T V L I Y F L P L L 210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V I G Y A Y T V V G I T L W A S E I P G 230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCCTCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTTC AGGATG 1766

Figure 23A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCAGAGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCTG 240
 41 G E G K V A T T V I S K M L F X E P I L 60
 241 GAGGTTTCCA GCTTGGCAG AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTG AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGNAATG 540
 141 V L G D A L V D F S L K L Y H A F S X M 160
 541 AAGAAGGTGG AGACCAACAT GGCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACAA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCCCTCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 23B

961 ACAACATTTG ATCCCAAGAA AACAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACATTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGTACCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG AACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACG AGCAGCACAA GTCCCTGTC TTCATGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTCTCT TAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AACCTGACA GACCAT 1826

Figure 24

1 TCCTCCACCT GCTGGCCCT GGACACCTCT GTCACCAGTG GTTCCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8

 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCAGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28

 121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATT CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68

 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACCGACGAAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

 301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108

 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128

 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCNA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T X E P E 148

 481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACCAAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168

 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C X K A 188

 601 CACGTCCAGA AGGTGACAGA CTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208

 661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228

 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248

 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262

 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 25A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCAGGG GGCGAAGGAA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 25B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGTT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 26A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGGCGA GACAGGCCCG GGTACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCAGGG GGCGAAGGAA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 26B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 27A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCCGA CCCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I V L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 27B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 28A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 ACCAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R K E V S R T 238

721 AGAGTGCAGGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 28B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 29A

1 ATGTTCTCTC CCTGGAAGAT ATCAAATGTTT CTGTCCTGTTT GTGAGGACTC CGTGCCCCACC 60
 1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACCA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 29B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGACTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTGCCCTGG GTTTCTTAA 1620

1621 TCTATTCAAG TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCAGTC CACCACAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

Figure 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCA 2280
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAACAG AGAAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

Figure 29D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGGGCCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCC 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAA AAA 3733

Figure 30A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCCTGTC GTGAGGACTC CGTGCCACC 60
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCCCTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTGAAA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCCTGG TTGTGCTGCT GCTATTCACTC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 30B

901 CTCTCCAGCT GCCAGGCAGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGTC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTGCCCTGG GTTTCTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

Figure 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGT AAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCAGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAAACCTGGAA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTG ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 30D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAA AAA 3733

Figure 31A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTG GTGAGGAAGT CGTGCCCACC 60
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCCCTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCCTGG TTGTGCTGCT GCTATTCATC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K E G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTGCCCTGG GTTTCTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

Figure 31C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATT A CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCA 2280
2281 CCACCCCTGAG GCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAACAG AGAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

Figure 31D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAAGAA CATCTGCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAA AAA 3733

Figure 32A

1	CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTAGTCTA	60
61	GGGAAAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTCCTG	120
1	M S S S S W	6
121	GCTCCTCTCAGCCTTGTTGCTGTAAGCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTGGACAAGTTAACCAATTACTGAAGAGAATGTCCAAACATGAATAATGCTGG	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAAATTATAACACCAATTACTGAAGAGAATGTCCAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTAAAGGAACAGTCCACACTTGCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAAGAACATCTCACAGTCAGCTCACAGCTGCAGGCTCTCAGCAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAACAGAGCAAACGGTTAACACAAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAACATGCTTATTACTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTGAATGAAATAATGGCAAACAGTTAGACTACAATGAGAGGCTCTGGCTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTGAAAGAGATTAACCATATATGAACATCTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

Figure 32B

901	GCTTGGTGATATGTGGGGTAGATTGGACAAATCTGTA	CTTGACAGTCCCTTG	960
267	L G D M W G R F W T N L Y S L T V P F G		286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGATGCACAGAG		1020
287	Q K P N I D V T D A M V D Q A W D A Q R		306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTGATCTGTTGGCTTCCTAATATGACTCAAGG		1080
307	I F K E A E K F F V S V G L P N M T Q G		326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTAGAAAGCAGTCTGCCATCC		1140
327	F W E N S M L T D P G N V Q K A V C H P		346
1141	CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT		1200
347	T A W D L G K G D F R I L M C T K V T M		366
1201	GGACGACTTCCTGACAGCTCATGAGATGGGCATATCCAGTATGATATGGCATATGC		1260
367	D D F L T A H H E M G H I Q Y D M A Y A		386
1261	TGCACAAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGGGG		1320
387	A Q P F L L R N G A N E G F H E A V G E		406
1321	AATCATGTCACTTTCTGCAAGCCACACCTAACGATTAAATCCATTGGTCTCTGTCACC		1380
407	I M S L S A A T P K H L K S I G L L S P		426
1381	CGATTTCAAGAAGACAATGAAACAGAAATAACTCCTGCTCAAACAAGCACTCACGAT		1440
427	D F Q E D N E T E I N F L L K Q A L T I		446
1441	TGTTGGACTCTGCCATTACTACATGTTAGAGAAGTGGAGGTGGATGGCTTTAAAGG		1500
447	V G T L P F T Y M L E K W R W M V F K G		466
1501	GGAAATTCCAAAGACCACTGGATGAAAAAGTGGTGGAGATGAAGCGAGAGATAGTTGG		1560
467	E I P K D Q W M K K W W E M K R E I V G		486
1561	GGTGGTGGAACCTGTGCCCATGATGAAACATACTGTGACCCCGCATCTGTTCCATGT		1620
487	V V E P V P H D E T Y C D P A S L F H V		506
1621	TTCTAATGATTACTCATTGATATTACACAAGGACCCTTACCAATTCCAGTTCA		1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q		526
1681	AGAAGCACTTGTCAAGCAGCTAACATGAAGGCCCTCTGCACAAATGTGACATCTCAA		1740
527	E A L C Q A A K H E G P L H K C D I S N		546

Figure 32C

1741	CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAGAATTCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTGGAGATAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAATCAGATGATTCTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTGAAACCAAGAACATCTCCTTAATTCTTTGTCAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAATGTGTCTGATATCATTCTAGAACTGAAGTGAAAAGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTCCGTCTGAATGACAACAGCCTAGAGTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTGGACCTCCTAACCGCCCCCTGTTCCATATGGCTGATTGTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGTAGTGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAGCAAGAACAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTCTCTTGAGGTGATTTGTTGTATGTAATGTTAATTCATGG	2580
2581	TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA	2640

Figure 32D

2641	AAAAAAATTGTCCAAAGACAAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTC	2700
2701	AGTATTTATTCTGTCTCTGGATTTGACTTCTGTTCTGTTCTTAATAAGGATTTGTAT	2760
2761	TAGAGTATATTAGGGAAAGTGTGTATTGGTCTCACAGGCTGTTAGGGATAATCTAAAT	2820
2821	GTAAATGTCTGTTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG	2880
2881	GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGAACTGGTAGC	2940
2941	TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCAATTAAATCCATTGTCAAGGATGA	3000
3001	CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTATTCACAGTGATGTT	3060
3061	GGAATCGATCATGCTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAACAG	3120
3121	GTAGAGGACATTGCTTTTCACTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA	3180
3181	AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTCTAC	3240
3241	TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACGTGATGTTCACCCCTCTGAAGTGGT	3300
3301	ACCCAGTCTCTAAATCTTGTATTTGCTCACAGTGTGAGCAGTGCTGAGCACAAAG	3360
3361	CAGACACTCAATAATGCTAGATTACACACTCAAAAAAAAAAA	3405

Figure 33A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTCGGAGACCCCAGGGAAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGCCCTACGCCATGCTTCCCTGGGGGCCTGCTCACACAGCCGAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTCTGGTAATTACATTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCTCAAGGACCACTCCAAAGACTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 33B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTCACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTCCTTGTGGTATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCCACGAAACCATAG 1284	
421	V V D P T K P * 428	

Figure 34A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCAGGGAAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGGCCTACGCCATGCTTCCCTGGGGCCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCCCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTCTGGTAATTACATTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCCCTCAAGGACCACTCCAAAGACTTTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 34B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTCACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCCACGAAACCATAG	1284
421	V V D P T K P *	428

Figure 35A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCAGGGAAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTGGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGCGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTGTGGATTACATTACTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCTCAAGGACCACTCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 35B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTCACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTGCCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTCCACCAGCACCCAGACTGTCTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG 1284	
421	V V D P T K P * 428	

Figure 36A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCAGGGAAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGGCCTACGCCATGCTTCCCTGGGGGCCTGCTCACACAGCCGAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCGATGCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAATTCCCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGNGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTGCTGGTAATTACATTACTTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCTCAAGGACCACCTCCAAAGACTTNTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 36B

841	CCTAACCAAGGC	AAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300	
901	TGGAACAACTTGTGCGGAAGAGGAATT	TTACAAGAACGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320	
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATT	TTGCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340	
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAA	ACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360	
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140	
361	K S F H K A T L D V D E A G T E A A A A	380	
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200	
381	T T F A I K F F S A Q T N R H I L R F N	400	
1201	CGGCCCTTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGGCAAG	1260	
401	R P F L V V I F S T S T Q S V L F L G K	420	
1261	GTCGTCGACCCCACGAAACCATAG	1284	
421	V V D P T K P *	428	

Figure 37A

1	CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTAGTCTA	60
61	GGGAAAGTCATTCACTGGATGTGATCTGGCTCACAGGGGACCATGTCAGCTCTCCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTGCTGTAAGTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTGGACAAGTTAACACAGCGAACGAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGATTATAACACCAATATTACTGAAGAGAAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTAAAGGAACAGTCCACACTGCCCCAATGTATCCACTACAA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAAGATCTCACAGTCAGCTCACAGCTGCAGGCTCTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGAACGGTTGAACACAATTCTAAATACAATGAGCACCATT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTGAAAGAGATTAAACCATTATATGAACATCTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

Figure 37B

901	GCTTGGT GATAT GTGGGG TAGAT TGGACAAATCTGTACTCTTGACAGTCCCTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTGTATCTGTTGGCTTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAAACCTTTCTGCTAACGAAATGGAGCTAACGATTCCATGAAGCTGTTGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTCTGCTAACGAAATGGAGCTAACGATTCCATGGTCTCTGTCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTCAAGAAGACAATGAAACAGAAATAACTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGACTCTGCCATTACTACATGTTAGAGAAGTGGAGGTGGATGGCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCCAAAGACCAGTGGATGAAAAGTGGTGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACCTGTGCCCATGATGAAACATACTGTGACCCCGCATCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTCAATTGATATTACACAAGGACCCTTACCAATTCCAGTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAACGACTTTGTCAAGCAGCTAACATGAAGGCCCTCTGCACAAATGTGACATCTCAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

Figure 37C

1741	CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTGGAAAATCAGAACCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAAGAATTCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGGAGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAATCAGATGATTCTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTGAAACCAAGAACATCTCCTTAATTCTTGTAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAACGTGTCTGATATCATTCTAGAACACTGAAGTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCCGGAGCCGTATCAATGATGCTTCCGTCTGAATGACAACAGCCTAGAGTTCTGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAAGCCCCCTGTTCCATATGGCTGATTGTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTATGGGAGTGTAGTAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAAGCAAGAACAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAAGACCTCCTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTCCCTTGTGAGGTGATTTGTTGTATGTAATGTTAATTCATGG	2580
2581	TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA	2640

Figure 37D

2641	AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC	2700
2701	AGTATTTATTCCTGTCCTGGATTGACTCTGTTCTGTTCTTAATAAGGATTGTAT	2760
2761	TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTCAGGGATAATCTAAAT	2820
2821	GTAAATGTCTGTTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG	2880
2881	GATCTTGTATGGAATATGGATGGATCACTTGTAAAGGACAGTGCCTGGAACTGGTAGC	2940
2941	TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCATTAAATCCATTGTCAAGGATGA	3000
3001	CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTATTGCCTACAGTGATGTT	3060
3061	GGAATCGATCATGCTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG	3120
3121	GTAGAGGACATTGCTTTCACTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA	3180
3181	AACTAGAGCCAGGGCCTCCGTAACTCCCAGAGCATGCCTGATAGAAACTCATTCTAC	3240
3241	TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACGTATGTTCACCCCTCTGAAGTGGT	3300
3301	ACCCAGTCTCTAAATCTTGCTCACAGTGTGAGCAGTGCTGAGCACAAAG	3360
3361	CAGACACTCAATAATGCTAGATTACACACTCAAAAAAAAAAA	3405

Figure 38A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCGTTN GTGAGGNCTC CGTGCCCACC 60
 1 M F S P W K I S M F L S V X E X S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCAG AGAACATCTT TGTCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCCTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCA 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GCCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCA 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 38B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K X G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q *

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCTGG GTTTCTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATT ATAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAAGT 2040

Figure 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATT A CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCAGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

D0053 NP

Figure 38D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAA AAA 3733

A

SNP1 (A/G)



SNP2 (G/C)

SNP2 (G/C)



SNP3 (C/A)



B

G G A

A C C

C

G C C

A G A

D

G G C

A C A

Figure 39

Figure 40

Father Mother

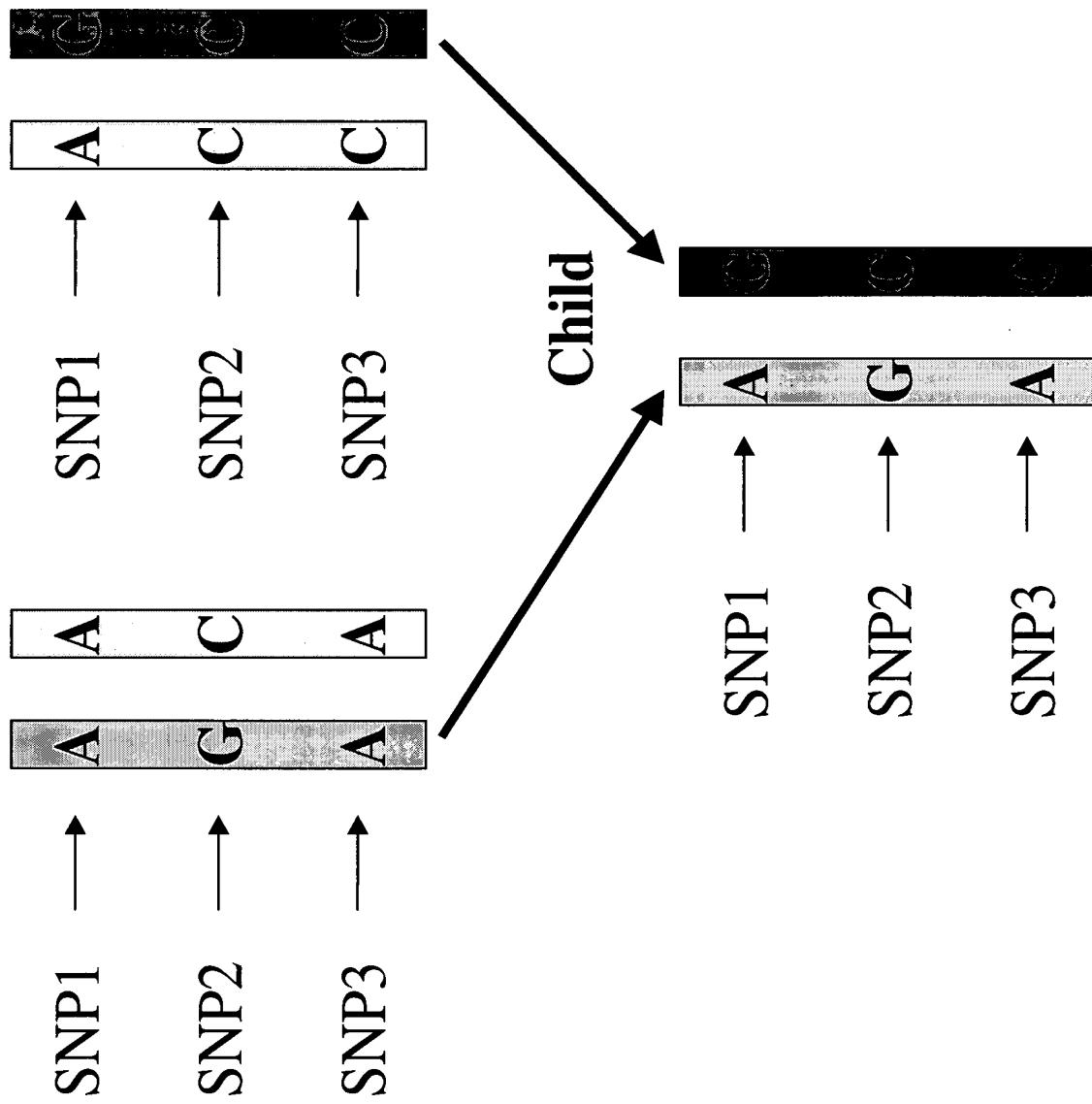


Figure 41A

1 CACCTATCC TACACTACTA GGAACTTGCA CAGTCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGGAGGAGC CCTCCCTCTC TCCCTGTCC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAAC TGCA GTGGTGA CTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCAACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCAGTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 41B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCATAAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCTAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTGGATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 41C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V *

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCTG 2520

2521 GGCCCCTAAT CCCAGGCCCT GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACCC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCATA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

D0053 NP

Figure 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 42A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGGGGAA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGC~~AGG~~ GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V Q G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

D0053 NP

Figure 42B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 43A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCGTTC GTGAGGCCTC CGTGCCCACC 60
 1 M F S P W K I S M F L S V R E A S V P T 20

61 ACGGCCTCTT TCAGGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCCCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGCCTTCC TGCTGCCCT GAGTGTCACTC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGGCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 43B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTAA 1620

1621 TCTATTCAAG TAGAACCTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCA 2280
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 43D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGGGCCC TATGCATGGT GTAGATGCC TGATAAAAGAA CATCTGCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAA AAA 3733

Figure 44A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGTGGATTACATTACTTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCAAGGACCACCTCCAAAGACTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCAATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 44B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACGACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTCCTTGTGGTGATCTTCCACCAGCACCCAGACTGTCTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCACGAAACCATAG 1284	
421	V V D P T K P * 428	

Figure 45A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCAGGGAAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGGCCTACGCCATGCTTCCCTGGGGCCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTAACCTCCCCGGCCATGGGCTGGAAACATGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T C V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCTGCACACTGTGGGCACAATCCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTGTGGATTACATTACTTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCAAGGACCACCTCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 45B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTCTACAAGAAGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCACGAAACCATAG	1284
421	V V D P T K P *	428

Figure 46A

1 CACCCATATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCCTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAAC TGCA GTGGTACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC **NGCTGGAGGG** 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 46B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCTAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V *

2341 GCTCCCCTCA CCCTGCCTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCT GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACCC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

D0053 NP

Figure 46D

2941 GAGGGAAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428